

FIG. 13A

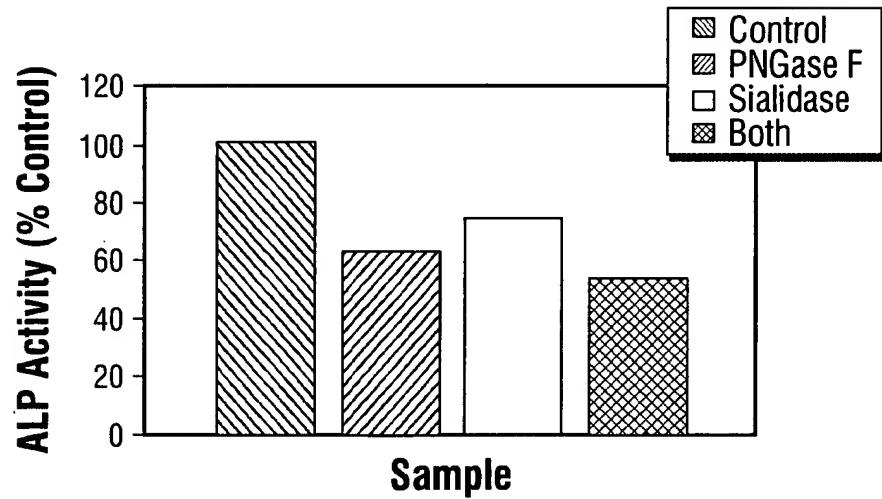


FIG. 13B



Identification of Proteins by Amino Acid Sequencing of Tryptic Fragments from 1D Gels

Band	Sample	Sequence Data	SEQ. ID NO:	Best Database Match	SEQ. ID NO:
1					
2	fx 49 (1579)	XLAAAGYDVEK	1	ALAAAGYDVEK	2
3	fx 67 (1346)	SLEKVCADLIR	3	SLEKVCADLIR	3
4	fx 65 ()	(Y)YCGMLGFPSEAPV	4	WCGMLGFPGEKRV	5
5	N terminal seq	STGVLLPLQNNELGP	6	STGVLLPLQNNELPG	6
	fx 72 (3925)	STGVLLPLQNNELPGAEYQY	7	STGVLLPLQNNELPGAEYQY	7
	fx 74 (3409)	STGVLLPLQ	8	STGVLLPLQ	8
6	fx 55 (1566)	(S)QTLQFXE	9	SQTLQFDE	10
	fx 47	YVAF	11	NO MATCH	
	N terminal seq	HAGKYSREKNT(P)A(P)	12	HGGKY'SREKNQPKP	13
	fx 57 (1438)	SQTLQFDEQ	14	SQTLQFDEQ	14
	fx 57 (1652)	SLKPSNHA	15	SLKPSNHA	15
7	fx 51 (1093)	AALRPLVKP	16	AALRPLVKP	16
	fx 37 (no MS)	A(H)(Q)VERVW	17	AIVER	18
	fx 37 (no MS)	A(H)(Q)VERVW	17	HQSDRYV	19
8	fx 78 ()	XALF(G)AQLGXALGP	20	NO MATCH	
9	fx 56 (1567)	SQTLQFDEQT	21	SQTLQFDEQT	21

FIG. 15A-1



Identification of Proteins by Amino Acid Sequencing of Tryptic Fragments from 1D Gels

Match	Identification	Species	Accession No.	AAs
11/11	Histone H1.c	human	876668 (NCBI)	65-75
11/11	40S Ribosomal Protein S20	rat	R3RT20 (PIR)	31-41
11/14	LORP	mouse	AAC95338 (NCBI)	213-226
15/15	BMP-3	human	4557371 (NCBI)	290-304
20/20	BMP-3	human	4557371 (NCBI)	290-309
9/9	BMP-3	human	4557371 (NCBI)	290-298
7/8	BMP-3	human	4557371 (NCBI)	346-353
	???			
11/14	α2-MACROGLOBULIN RECEPTOR ASSOC. PRO.	human	P30533 (Swiss-Prot)	31-46
9/9	BMP-3	human	4557371 (NCBI)	346-354
8/8	BMP-3	human	4557371 (NCBI)	410-417
9/9	60S Ribosomal Protein L32	mouse	P17932 (Swiss-Prot)	1-9
5/5	60S Ribosomal Protein L32	mouse	P17932 (Swiss-Prot)	109-113
5/7	60S Ribosomal Protein L32	mouse	P17932 (Swiss-Prot)	22-28
	???			
10/10	BMP-3	human	P12645 (Swiss-Prot)	346-355

FIG. 15A-2



Identification of Proteins by Amino Acid Sequencing of Tryptic Fragments from 1D Gels

Band	Sample	Sequence Data	SEQ. ID NO:	Best Database Match	SEQ. ID NO:
11	fx 55 (1311)	SQTLXF	22	SQTLQF	23
	fx 47 (1772)	VLATVTKPVGGDK	24	VLATVTKPVGGDK	24
	fx 76 (1795)	xVFAL	25	VFAL	25
	fx 61 (1145)	AVPQLQGYLR	26	AIPQLQGYLR	27
18					
22	fx 58 (1101)	ALDAAYCFR	28	ALDAAYCFR	28
	fx 69 (NO MATCH)	GYNANFCAGACPYL	29	GYNANFCAGACPYL	29
	fx 66 (1411.71)	VNSQSLSPY	30	VNSQSLSPY	30
25	fx 39 (1470)	KAAKPSV(P)	31	KAAKPSV(P)	31
29					

FIG. 15B-1



Identification of Proteins by Amino Acid Sequencing of Tryptic Fragments from 1D Gels

Match	Identification	Species	Accession No.	As
5/6	BMP-3	human	45557371 (NCBI)	346-351
13/13	60s Ribosomal Protein L6	human	Q02878 (Swiss-Prot)	87-99
4/4	60s Ribosomal Protein L6	human	Q02878 (Swiss-Prot)	273-276
9/10	60s Ribosomal Protein L6	human	Q02878 (Swiss-Prot)	262-271
9/9	TGF- β 2	human	P08112 (Swiss-Prot)	303-311
14/14	TGF- β 2	human	P08112 (Swiss-Prot)	340-353
9/9	SPP24	bovine	Q27967 (Swiss-Prot)	42-50
8/8	Histone H1 x	human	JC4928 (PIR)	199-206

FIG. 15B-2



Identifications of Proteins by Mass Spectrometry of Fragments from 2D Gels

FIG. 19B

Identifications of Proteins by Mass Spectrometry of Fragments from 2D Gels



SPAL	DIGEST	MASS SPEC PROFILE	SPECIES	ACC. NO.	MS PEAKS			AAS	% COVERAGE	COMMENTS
					DATA	DATABASE	DIFF			
9	TRYPSIN	7 PEAKS MATCH WITH RIBOSOME S3s	MOUSE	P97351 (SWISS-PROT)	920.05	920.10	-0.05	19-25	29	
					1218.29	1218.31	-0.02	152-161		
					1346.62	1346.49	0.13	151-161		
					1516.69	1516.69	0.00	174-166		
					1593.72	1523.82	-0.10	94-106		
					1719.91	1720.00	-0.09	199-212		
					1953.12	1953.16	-0.04	65-81		
					1327.75	1327.68	0.19	34-46	23	
10	TRYPSIN	4 PEAKS MATCH WITH RIBOSOME H1.c	HUMAN	87658 (NCBI)						
					1579.70	1579.71	-0.01	65-78		
					1707.65	1707.89	-0.24	64-79		
					2147.17	2147.53	-0.36	1-21		
					1168.46	1168.33	0.10	230-239	23	
11	TRYPSIN	6 PEAKS MATCH WITH RIBOSOME S4	HUMAN	P12750 (SWISS-PROT)						
					1215.39	1216.39	0.00	134-144		
					1354.03	1353.61	0.42	230-241		
					1507.86	1507.88	0.12	198-210		
					1557.75	1557.98	-0.23	37-48		
					2140.34	2140.58	-0.24	221-239		
					2591.60	2591.90	-0.10	77-98		

FIG. 19C